

## RAW SEQUENCE LISTING

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Application Serial Number: 10/537,075

Source: PCT/10

Date Processed by STIC: 6/13/05

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PCT

## RAW SEQUENCE LISTING

DATE: 06/13/2005

PATENT APPLICATION: US/10/537,075

TIME: 09:38:34

Input Set : A:\12810-91 Sequence Listing.txt

Output Set: N:\CRF4\06132005\J537075.raw

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3 <110> APPLICANT: Kessler, Maria
4     Zelinski, Thomas
5     Hauer, Bernhard
7 <120> TITLE OF INVENTION: L-RHAMNOSE-INDUCIBLE EXPRESSION SYSTEMS
9 <130> FILE REFERENCE: 12810-00091-US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/537,075
C--> 11 <141> CURRENT FILING DATE: 2005-06-01
11 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/013367
12 <151> PRIOR FILING DATE: 2003-11-27
14 <150> PRIOR APPLICATION NUMBER: DE 102 56 381.0
15 <151> PRIOR FILING DATE: 2002-12-02
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2046
23 <212> TYPE: DNA
24 <213> ORGANISM: Escherichia coli
26 <220> FEATURE:
27 <221> NAME/KEY: misc_feature
28 <222> LOCATION: (288)..(1121)
29 <223> OTHER INFORMATION: coding for rhaS (positive regulator of rhaBAD operon)
31 <220> FEATURE:
32 <221> NAME/KEY: misc_feature
33 <222> LOCATION: (1108)..(2043)
34 <223> OTHER INFORMATION: coding for rhaR (positive regulator of rhaRS operon)
36 <220> FEATURE:
37 <221> NAME/KEY: protein_bind
38 <222> LOCATION: (56)..(72)
39 <223> OTHER INFORMATION: potential RhaS binding site
41 <220> FEATURE:
42 <221> NAME/KEY: protein_bind
43 <222> LOCATION: (89)..(105)
44 <223> OTHER INFORMATION: potential RhaS binding site
46 <220> FEATURE:
47 <221> NAME/KEY: protein_bind
48 <222> LOCATION: (172)..(203)
49 <223> OTHER INFORMATION: potential RhaR binding site
51 <220> FEATURE:
52 <221> NAME/KEY: protein_bind
53 <222> LOCATION: (210)..(241)
54 <223> OTHER INFORMATION: potential RhaR binding site
56 <220> FEATURE:
57 <221> NAME/KEY: misc_feature

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58 &lt;222&gt; LOCATION: (24)

59 &lt;223&gt; OTHER INFORMATION: potential start of transcription (complement)

W--&gt; 60 &lt;400&gt; SEQUENCE: 1

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61 aatgtgatcc tgctgaattt cattacgacc agtctaaaaa gcgccctgaat tcgcgacctt 60
62 ctcgttactg acaggaaaat gggccattgg caaccaggga aagatgaacg tgatgatgtt 120
63 cacaatttgc tgaattgtgg tgatgtgatg ctccaccgat ttcctgaaaaa ttcacgctgt 180
64 atcttgaaaa atcgacgttt ttacgtggg tttccgtcga aaatttaagg taagaacctg 240
65 acctcgtgat tactatttcg ccgtgttgac gacatcagga ggccagtatg accgtattac 300
66 atagtgtgga tttttttccg tctggtaacg cgtccgtggc gatagaacct cggctcccgc 360
67 aggcgattt tcctgaacat catcatgatt ttcattgaaat tgtgattgtc gaacatggca 420
68 cgggtattca tgtgtttaat gggcagccct ataccatcac cgggtggcacg gtctgtttcg 480
69 tacgcatca tgatcggcat ctgtatgaac ataccgataa tctgtgtctg accaatgtgc 540
70 tgatcgctc gccggatcga tttcagtttc tcgcccgggt gaatcagttg ctgccacaag 600
71 agctggtgg gcagtatccg tctcactggc gcgttaacca cagcgtattg cagcaggtgc 660
72 gacagctggg tgcacagatg gaacagcagg aaggggaaaa tgatttacc tgcaccgcca 720
73 gtcgcgagat cttgtttatg caattactgc tcttgctgcg taaaagcagt ttgcaggaga 780
74 acctggaaaa cagcgcacat cgtctcaact tgcttctggc ctggctggag gaccattttg 840
75 ccgatgaggt gaattgggat gccgtggcgg atcaattttc tctttcactg cgtacgctac 900
76 atcggcagct taagcagcaa acgggactga cgcctcagcg atacctgaac cgcctgcgac 960
77 tgatgaaagc ccgacatctg ctacgccaca gcgaggccag cgttactgac atcgccatc 1020
78 gctgtggatt cagcgacagt aaccactttt cgacgctttt tcgccgagag ttaactggg 1080
79 caccgctga tattcgccag ggacgggatg gctttctgca ataacgcgaa tcttctcaac 1140
80 gtatttgtac gccatattgc gaataatcaa cttcgttctc tggccgaggt agccacgggt 1200
81 gcgcacagt taaaacttct caaagatgat ttttttgcca gcgaccagca ggcatcgct 1260
82 gtggctgacc gttatccgca agatgtcttt gctgaacata cacatgattt ttgtgagctg 1320
83 gtgattgtct ggcgcggtaa tggcctgcat gtactcaacg atcgccctta tcgcattacc 1380
84 cgtggcgatc tcttttacat tcatgctgac gataaacact cctacgcttc cgtaaacgat 1440
85 ctggttttgc agaataattt ttattgcccg gagcgtctga agctgaatct tgactggcag 1500
86 gggcgattc cgggatttaa cgccagcgca gggcaaccac actggcgctt aggtagcatg 1560
87 gggatggcgc aggcgcggca ggttatcggt cagcttgagc atgaaagtag tcagcatgtg 1620
88 ccgtttgcta acgaaatggc tgagttgtct ttcgggcagt tggatgatgt gctgaatcgc 1680
89 catcgttaca ccagtgattc gttgccgcca acatccagcg aaacggttgc ggataagctg 1740
90 attacccggc tggcggttag cctgaaaagt ccctttgcgc tggataaatt ttgtgatgag 1800
91 gcatcgtgca gtgagcgcgt tttgcgtcag caatttcgcc agcagactgg aatgaccatc 1860
92 aatcaatatc tgcgacaggt cagagtgtgt catgcgcaat atcttctcca gcatagccgc 1920
93 ctgttaatca gtgatatttc gaccgaatgt ggctttgaag atagtaacta ttttcgggtg 1980
94 gtgtttaccg gggaaaccgg gatgacgccc agccagtggc gtcactctca ttcgcagaaa 2040
95 gattaa 2046

```

98 &lt;210&gt; SEQ ID NO: 2

99 &lt;211&gt; LENGTH: 287

100 &lt;212&gt; TYPE: DNA

101 &lt;213&gt; ORGANISM: Escherichia coli

W--&gt; 102 &lt;220&gt; FEATURE:

103 &lt;221&gt; NAME/KEY: promoter

104 &lt;222&gt; LOCATION: (1)..(287)

105 &lt;223&gt; OTHER INFORMATION: rhaBAD promoter fragment containing rhaS and rhaR binding sites

W--&gt; 106 &lt;400&gt; SEQUENCE: 2

```

107 actggcctcc tgatgtcgtc aacacggcga aatagtaatc acgaggtcag gttcttacct 60
108 taaattttcg acggaaaacc acgtaaaaaa cgctcgattt tcaagataca gcgtgaattt 120

```

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```

109 tcaggaaatg cggtagcat cacatcacca caattcagca aattgtgaac atcatcacgt 180
110 tcatctttcc ctggttgcca atggccatt ttcctgtcag taacgagaag gtcgcgaatt 240
111 caggcgcttt ttagactggt cgtaatgaaa ttcagcagga tcacatt 287
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 125
116 <212> TYPE: DNA
117 <213> ORGANISM: Escherichia coli
W--> 118 <220> FEATURE:
119 <221> NAME/KEY: promoter
120 <222> LOCATION: (1)..(125)
121 <223> OTHER INFORMATION: rhaBAD promoter fragment containing RhaS binding site
W--> 122 <400> SEQUENCE: 3
123 ttgtgaacat catcacgttc atctttccct ggttgccaat ggccatttt cctgtcagta 60
124 acgagaaggt cgcgaattca ggcgcttttt agactggtcg taatgaaatt cagcaggatc 120
125 acatt 125
128 <210> SEQ ID NO: 4
129 <211> LENGTH: 123
130 <212> TYPE: DNA
131 <213> ORGANISM: Escherichia coli
W--> 132 <220> FEATURE:
133 <221> NAME/KEY: promoter
134 <222> LOCATION: (1)..(123)
135 <223> OTHER INFORMATION: rhaBAD promoter fragment containing RhaS binding site
W--> 136 <400> SEQUENCE: 4
137 atcaccacaa ttcagcaaat tgtgaacatc atcacgttca tctttccctg gttgccaatg 60
138 gccatttttc ctgtcagtaa cgagaaggtc gcgaattcag gcgcttttta gactggtcgt 120
139 aat 123
142 <210> SEQ ID NO: 5
143 <211> LENGTH: 51
144 <212> TYPE: DNA
145 <213> ORGANISM: Escherichia coli
W--> 146 <220> FEATURE:
147 <221> NAME/KEY: misc_feature
148 <222> LOCATION: (1)..(51)
149 <223> OTHER INFORMATION: palindromic RhaS binding site of rhaBAD promoter
W--> 150 <400> SEQUENCE: 5
151 atctttccct ggttgccaat ggccatttt cctgtcagta acgagaaggt c 51
154 <210> SEQ ID NO: 6
155 <211> LENGTH: 1071
156 <212> TYPE: DNA
157 <213> ORGANISM: Alcaligenes faecalis
W--> 158 <220> FEATURE:
159 <221> NAME/KEY: CDS
160 <222> LOCATION: (1)..(1068)
161 <223> OTHER INFORMATION: coding for nitrilase
W--> 162 <400> SEQUENCE: 6
163 atg cag aca aga aaa atc gtc cgg gca gcc gcc gta cag gcc gcc tct 48
164 Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
165 1 5 10 15

```

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166 ccc aac tac gat ctg gca acg ggt gtt gat aaa acc att gag ctg gct 96
167 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
168          20          25          30
169 cgt cag gcc cgc gat gag ggc tgt gac ctg atc gtg ttt ggt gaa acc 144
170 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
171          35          40          45
172 tgg ctg ccc gga tat ccc ttc cac gtc tgg ctg ggc gca ccg gcc tgg 192
173 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
174          50          55          60
175 tcg ctg aaa tac agt gcc cgc tac tat gcc aac tcg ctc tcg ctg gac 240
176 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
177 65          70          75          80
178 agt gca gag ttt caa cgc att gcc cag gcc gca cgg acc ttg ggt att 288
179 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
180          85          90          95
181 ttc atc gca ctg ggt tat agc gag cgc agc ggc ggc agc ctt tac ctg 336
182 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
183          100          105          110
184 ggc caa tgc ctg atc gac gac aag ggc gag atg ctg tgg tcg cgt cgc 384
185 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
186          115          120          125
187 aaa ctc aaa ccc acg cat gta gag cgc acc gta ttt ggt gaa ggt tat 432
188 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
189          130          135          140
190 gcc cgt gat ctg att gtg tcc gac aca gaa ctg gga cgc gtc ggt gct 480
191 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
192 145          150          155          160
193 cta tgc tgc tgg gag cat ttg tcg ccc ttg agc aag tac gcg ctg tac 528
194 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
195          165          170          175
196 tcc cag cat gaa gcc att cac att gct gcc tgg ccg tcg ttt tcg cta 576
197 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
198          180          185          190
199 tac agc gaa cag gcc cac gcc ctc agt gcc aag gtg aac atg gct gcc 624
200 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
201          195          200          205
202 tcg caa atc tat tcg gtt gaa ggc cag tgc ttt acc atc gcc gcc agc 672
203 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser
204          210          215          220
205 agt gtg gtc acc caa gag acg cta gac atg ctg gaa gtg ggt gaa cac 720
206 Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu His
207 225          230          235          240
208 aac gcc ccc ttg ctg aaa gtg ggc ggc ggc agt tcc atg att ttt gcg 768
209 Asn Ala Pro Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe Ala
210          245          250          255
211 ccg gac gga cgc aca ctg gct ccc tac ctg cct cac gat gcc gag ggc 816
212 Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu Gly
213          260          265          270
214 ttg atc att gcc gat ctg aat atg gag gag att gcc ttc gcc aaa gcg 864

```

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215 Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys Ala
216          275          280          285
217 atc aat gac ccc gta ggc cac tat tcc aaa ccc gag gcc acc cgt ctg 912
218 Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg Leu
219          290          295          300
220 gtg ctg gac ttg ggg cac cga gac ccc atg act cgg gtg cac tcc aaa 960
221 Val Leu Asp Leu Gly His Arg Asp Pro Met Thr Arg Val His Ser Lys
222 305          310          315          320
223 agc gtg acc agg gaa gag gct ccc gag caa ggt gtg caa agc aag att 1008
224 Ser Val Thr Arg Glu Ala Pro Glu Gln Gly Val Gln Ser Lys Ile
225          325          330          335
226 gcc tca gtc gct atc agc cat cca cag gac tcg gac aca ctg cta gtg 1056
227 Ala Ser Val Ala Ile Ser His Pro Gln Asp Ser Asp Thr Leu Leu Val
228          340          345          350
229 caa gag ccg tct tga 1071
230 Gln Glu Pro Ser
231          355
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 356
236 <212> TYPE: PRT
237 <213> ORGANISM: Alcaligenes faecalis
W--> 238 <400> SEQUENCE: 7
239 Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala Ser
240 1          5          10          15
241 Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu Ala
242          20          25          30
243 Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu Thr
244          35          40          45
245 Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala Trp
246          50          55          60
247 Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu Asp
248 65          70          75          80
249 Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly Ile
250          85          90          95
251 Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr Leu
252          100          105          110
253 Gly Gln Cys Leu Ile Asp Asp Lys Gly Glu Met Leu Trp Ser Arg Arg
254          115          120          125
255 Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly Tyr
256          130          135          140
257 Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly Ala
258 145          150          155          160
259 Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu Tyr
260          165          170          175
261 Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser Leu
262          180          185          190
263 Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala Ala
264          195          200          205
265 Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala Ser

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## VERIFICATION SUMMARY

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Input Set : A:\12810-91 Sequence Listing.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:60 M:283 W: Missing Blank Line separator, <400> field identifier  
L:102 M:283 W: Missing Blank Line separator, <220> field identifier  
L:106 M:283 W: Missing Blank Line separator, <400> field identifier  
L:118 M:283 W: Missing Blank Line separator, <220> field identifier  
L:122 M:283 W: Missing Blank Line separator, <400> field identifier  
L:132 M:283 W: Missing Blank Line separator, <220> field identifier  
L:136 M:283 W: Missing Blank Line separator, <400> field identifier  
L:146 M:283 W: Missing Blank Line separator, <220> field identifier  
L:150 M:283 W: Missing Blank Line separator, <400> field identifier  
L:158 M:283 W: Missing Blank Line separator, <220> field identifier  
L:162 M:283 W: Missing Blank Line separator, <400> field identifier  
L:238 M:283 W: Missing Blank Line separator, <400> field identifier  
L:291 M:283 W: Missing Blank Line separator, <220> field identifier  
L:295 M:283 W: Missing Blank Line separator, <400> field identifier  
L:382 M:283 W: Missing Blank Line separator, <400> field identifier  
L:442 M:283 W: Missing Blank Line separator, <220> field identifier  
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L:947 M:283 W: Missing Blank Line separator, <220> field identifier  
L:951 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1024 M:283 W: Missing Blank Line separator, <400> field identifier